

[0142] As used herein, "force-activated bond stress-dependent adhesion molecule" and "FABSDAM" refer to molecules that are capable of binding ligands in a force-activated bond stress-dependent manner. FABSDAMs include, but are not limited to, adhesins, selectins, and integrins. Adhesion molecules include adhesins, selectins, integrins, cadherins, immunoglobulin superfamily cell adhesion molecules, and syndecans (Hauck C. R. (2002) *Med Microbiol. Immuno.* 191:55-62). FimH proteins are adhesins of bacterial origin. FimH polypeptides include all proteins that are structurally and functionally similar to bacterial derived FimH proteins, including, but not limited to all natural bacterial FimH variants, purified natural FimH proteins, engineered FimH polypeptides, mutated FimH polypeptides, chemically synthesized FimH polypeptides, and truncated but functional portions that are polypeptides of FimH proteins such as the lectin domain. FimH sequences can be found at GenBank Accession Nos. X05672 and AF288194. Methods for purifying FimH are known in the art (see Jones, 1995). As used herein, "isolated force-activated bond stress-dependent binding adhesion molecule" and "I-FABSDAM" refer to FABSDAMs that are not in the same context in which they exist in nature, including their natural in vivo context. All I-FABSDAMs are FABSDAMs. An *E. coli* that naturally has FimH-j96 protein, a naturally occurring variant of FimH, that has been transformed with an engineered FimH-f18 gene, isolated from a naturally occurring *E. coli* variant, and expresses FimH-f18, comprises two FABSDAMs but only one I-FABSDAM. Both FimH-j96 protein and FimH-f18 protein are FABSDAMs, but only the engineered and transformed FimH-f18 protein is an I-FABSDAM in this example. Even if the FimH-f18 (FimH-f18 is a natural strain) protein has the same sequence as the naturally occurring variant, because it is not in the in vivo context in which it is found in nature, it is isolated. Adhesins also include extracellular matrix adhesins, for example collagen adhesins of *S. aureus* which bind to collagen.

6 Review: 0

Items 1 - 6 of 6

One page.

1: Brooks DE, Trust TJ.

Related Articles, Links



Enhancement of bacterial adhesion by shear forces: characterization of the haemagglutination induced by *Aeromonas salmonicida* strain 438. *J Gen Microbiol.* 1983 Dec;129(12):3661-9.

PMID: 6668467 [PubMed - indexed for MEDLINE]

Q21 J4

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*Am Rev Respir Dis.* 1983 Jul;128(1):50-3.

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Related Articles, Links

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*Micrleen*

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Related Articles, Links

Therapeutic plasmapheresis in patients with antibodies to high-frequency red cell antigens.

*Prog Clin Biol Res.* 1982;106:347-53. No abstract available.

PMID: 7178141 [PubMed - indexed for MEDLINE]

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L20: Entry 9 of 16

File: USPT

Nov 1, 2005

DOCUMENT-IDENTIFIER: US 6960457 B1

TITLE: Reversible immobilization of arginine-tagged moieties on a silicate surface

Detailed Description Text (3):

This invention, is premised, in part, on the discovery that an arginine tag (e.g., a single arginine or a series of arginine molecules covalently linked together) will interact with the surface of layered silicates (i.e., negatively charged layered silicates such as mica) and form a highly specific interaction with the layered silicate surface. Without being bound to a particular theory, it is believed that the guanidino group (—NH—C(.dbd.NH)—NH<sub>2</sub>) of the arginine participates in a cation exchange with the layered silicate surface. The reaction, however, appears to be more specific than a simple ion exchange (possibly involving precise steric relationships) and consequently, the adhesion is substantially more resistant to dissociation by various cations such as sodium. Thus, the attachment is stable to physiologically relevant concentrations of cations such as Mg<sup>2+</sup> (10 mM or greater), Na<sup>+</sup> (100 mM or greater), and so forth.

Other Reference Publication (103):

Spudich et al. (1996) "Effect of different surfaces and binding modes on the velocity of a single-headed myosin fragment in the *vitro* motility assay," Mol. Biol. of the Cell 7:35a, Abstract 206.

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US 20030104492A1

(19) United States

(12) Patent Application Publication (10) Pub. No.: US 2003/0104492 A1  
Chu (43) Pub. Date: Jun. 5, 2003

(54) FLOW-THROUGH MEMBRANE ASSAYS  
FOR CARBOHYDRATES USING LABELED  
LECTINS

(52) U.S. Cl. .... 435/7.9

(76) Inventor: Albert Chu, Hillsborough, CA (US)

(57)

### ABSTRACT

Correspondence Address:  
David J. Brezner, Esq.  
FLEHR HOHBACH TEST  
ALBRITTON & HERBERT LLP  
Four Embarcadero Center, Suite 3400  
San Francisco, CA 94111-4187 (US)

(21) Appl. No.: 10/023,205

(22) Filed: Dec. 14, 2001

#### Related U.S. Application Data

(60) Provisional application No. 60/256,143, filed on Dec. 15, 2000.

#### Publication Classification

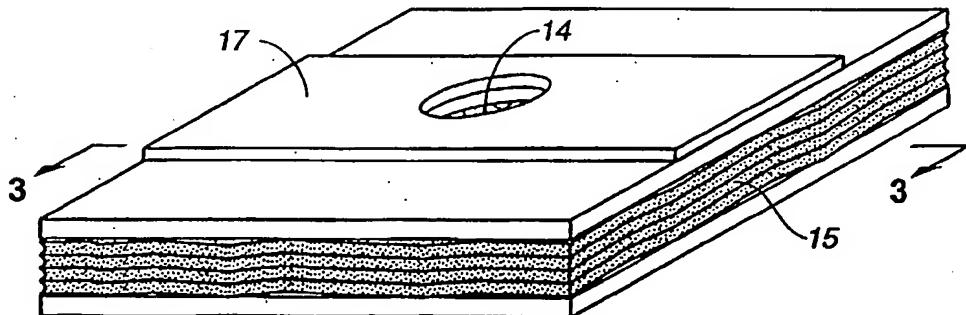
(51) Int. Cl. 7 G01N 33/53; G01N 33/542

The present invention comprises a method for rapid detection of at least a first carbohydrate in a carbohydrate-containing sample molecule comprising the steps of:

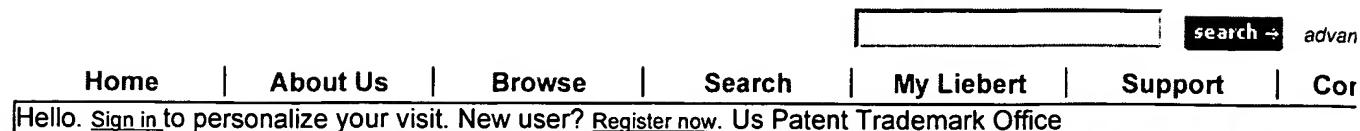
(a) retaining the sample molecule on a region of one liquid permeable reaction membrane,

(b) flowing a solution of first lectin, capable of binding the first carbohydrate, through the one reaction membrane to bind the first lectin to the retained first carbohydrate, the lectin being directly conjugated to a label prior to binding to the carbohydrate or being bound to a labeled separate molecule only after the first lectin has been bound to the carbohydrate, and

(c) thereafter, detecting the label bound on the one reaction membrane, indicating the presence of the first carbohydrate.



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## ASSAY and Drug Development Technologies

### Quantification of Small Molecule-Receptor Affinities and Kinetics by Acoustic Profiling

Oct 2006, Vol. 4, No. 5 : 565 -573

**Xin Li**

Akubio Ltd., Cambridge, UK.

**Kevin S. J. Thompson**

Akubio Ltd., Cambridge, UK.

**Ben Godber**

Akubio Ltd., Cambridge, UK.

**Matthew A. Cooper, Ph.D.**

Akubio Ltd., Cambridge, UK.

The label-free RAP<sup>id</sup> 4™ system that exploits resonant acoustic profiling (RAP™) from Akubio (Cambridge, UK) was used to determine the affinity and kinetics for several different small molecule–receptor interactions. This was achieved by attaching the target receptor to the surface of quartz crystal resonators through a variety of specific coupling chemistries, followed by application of a small-molecular-weight ligand to the receptor via a microfluidic flow-based delivery system. Rank order of binding was determined for very weak interactions such as cofactor binding to glucose dehydrogenase. Moderate interaction affinities and binding kinetics could be determined for biotin binding to a specific antibody, and also for several low-molecular-weight sulfonamide analogues binding to human carbonic anhydrase isoform II. The equilibrium binding constants were in general agreement with the values obtained by kinetic analysis of the data, as well as with previously published values obtained using surface plasmon resonance, stopped flow fluorescence, and isothermal titration calorimetry.

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: J Gen Microbiol. 1983 Dec;129(12):3661-9.

Links

**Enhancement of bacterial adhesion by shear forces: characterization of the haemagglutination induced by *Aeromonas salmonicida* strain 438.**

**Brooks DE, Trust TJ.**

Application of a viscometric assay to the haemagglutination induced by *Aeromonas salmonicida* strain 438 showed that shear forces can enhance the strength of bacterial adhesion. The D-mannose/L-fucose-sensitive reaction proceeded in two phases, an initial phase in which the degree of aggregation remained constant during shearing and a second stage, induced by shear, in which agglutination was enhanced as shear was maintained. The results strongly paralleled those found in studies of concanavalin A-induced haemagglutination, providing good evidence that adhesion in this species took place via lectin-like molecules. Methyl-alpha-D-mannoside, which strongly inhibits haemagglutination in this system, would not fully reverse the shear-dependent reaction. EGTA inhibited and reversed both phases, however. The effects of bacterial concentration, temperature, time of growth, pH, and a spectrum of monosaccharide inhibitors were also studied. The results demonstrated that the shear-dependent reaction has a number of features which distinguish it from the initial stage of haemagglutination, implying differences in the underlying biochemical mechanisms involved.

PMID: 6668467 [PubMed - indexed for MEDLINE]

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END OF SEARCH HISTORY



US007054768B2

(12) **United States Patent**  
Anderson

(10) **Patent No.:** US 7,054,768 B2  
(45) **Date of Patent:** May 30, 2006

(54) **METHOD AND SYSTEM FOR SHEAR FLOW PROFILING**

(75) Inventor: Erik J. Anderson, Cambridge, MA (US)

(73) Assignee: Woods Hole Oceanographic Institution, Woods Hole, MA (US)

(\*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 26 days:

(21) Appl. No.: 10/875,051

(22) Filed: Jun. 22, 2004

(65) **Prior Publication Data**

US 2005/0283323 A1 Dec. 22, 2005

(51) **Int. Cl.**

G01F 17/00 (2006.01)

(52) **U.S. Cl.** 702/50; 405/52; 382/107

(58) **Field of Classification Search** 702/50;

405/79, 52, 80; 472/128; 382/107

See application file for complete search history.

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(Continued)

*Primary Examiner*—John Barlow

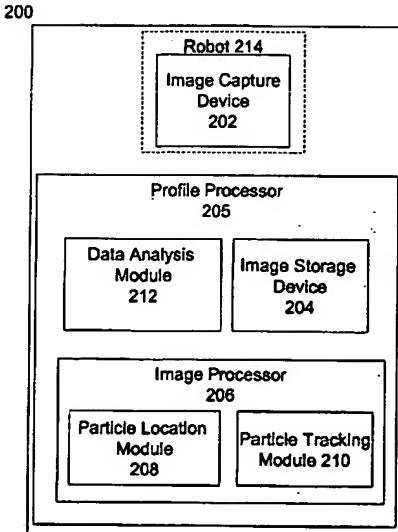
*Assistant Examiner*—Hien Vo

(74) *Attorney, Agent, or Firm*—Fish & Neave IP Group Ropes & Gray LLP

(57) **ABSTRACT**

The invention relates to a computerized method of profiling a shear flow, such as a boundary layer. The method includes receiving two successive images of a plurality of particles in the shear flow near the interface being analyzed. The method also includes determining a set of potential particle motion vectors based on the received images and dynamically ranks the likelihood that the potential tracks are correct based on track density. Track density is calculated using a plot matrix and kernel technique. The ranking is used to match particles from the successive images. The method also includes generating a velocity profile of the flow about the interface based on the particles matches and the determined location of the interface. The method is also applicable to moving and deforming interfaces.

41 Claims, 11 Drawing Sheets



[0013] According to a preferred embodiment of the present invention, the probe is moved at a advance velocity which is lower than or equal to a reference velocity that is determined by the physiological binding rate for natural cell movement of biological cells (binding velocity of the cells). The natural cell movement (cell locomotion) comprises the change in location of a complete cell on a fixed surface or in cell material by rearranging adhesion contacts of cell organs (membrane organs, for example, membrane protuberances), as are described, for example, by M. Abercrombie et al. in the publication "The Locomotion Of Fibroblasts In Culture" ("Experimental Cell Research", Vol. 67, 1971, pages 359-367) and by L. P. Cramer in the publication "Organization and polarity of actin filament networks in cells: implications for the mechanism of myosin-based cell motility" ("Biochem. Soc. Symp." Vol. 65, 1999, pages 173-205).

0015] The physiological reference velocity is known per se (see, for example, G. Fuhr et al. in "Biol. Chem.", 1998, Vol. 379, pages 1161-1173) or measurable on animal or human cells. The binding rate of interest may be derived by measuring the dynamics of adhesion patterns of individual cells on artificial surfaces, for example.



US 20040191246A1

(19) **United States**

(12) **Patent Application Publication** (10) **Pub. No.: US 2004/0191246 A1**  
Connelly et al. (43) **Pub. Date: Sep. 30, 2004**

(54) **PROCESS FOR IN VIVO TREATMENT OF  
SPECIFIC BIOLOGICAL TARGETS IN  
BODILY FLUID**

(76) Inventors: **Patrick R. Connelly**, Rochester, NY  
(US); **Jeffrey L. Helfer**, Webster, NY  
(US); **Andrew W. Custer**, Davis, CA  
(US); **Michael B. Klm**, Boston, MA  
(US)

Correspondence Address:  
**HOWARD J. GREENWALD P.C.**  
**349 W. COMMERCIAL STREET SUITE 2490**  
**EAST ROCHESTER, NY 14445-2408 (US)**

(21) Appl. No.: **10/787,279**

(22) Filed: **Feb. 26, 2004**

**Related U.S. Application Data**

(63) Continuation-in-part of application No. 60/450,450,  
filed on Feb. 26, 2003.

**Publication Classification**

(51) Int. Cl. <sup>7</sup> ..... **A61K 39/395**  
(52) U.S. Cl. ..... **424/140.1**

(57) **ABSTRACT**

A process for the in vivo treatment of the bodily fluid of a biological organism is presented, wherein the organism is implanted with a capture device containing a target specific binding agent. The bodily fluid of the donor is brought into contact with the binding agent and the desired cellular components are allowed to bind with the binding agent.



US 20050283323A1

(19) **United States**

(12) **Patent Application Publication** (10) **Pub. No.: US 2005/0283323 A1**  
Anderson (43) **Pub. Date: Dec. 22, 2005**

(54) **METHOD AND SYSTEM FOR SHEAR FLOW PROFILING** (52) **U.S. Cl. .... 702/50**

(76) **Inventor: Erik J. Anderson, Cambridge, MA (US)** (57) **ABSTRACT**

**Correspondence Address:**  
**FISH & NEAVE IP GROUP**  
**ROPES & GRAY LLP**  
**ONE INTERNATIONAL PLACE**  
**BOSTON, MA 02110-2624 (US)**

(21) **Appl. No.: 10/875,051**

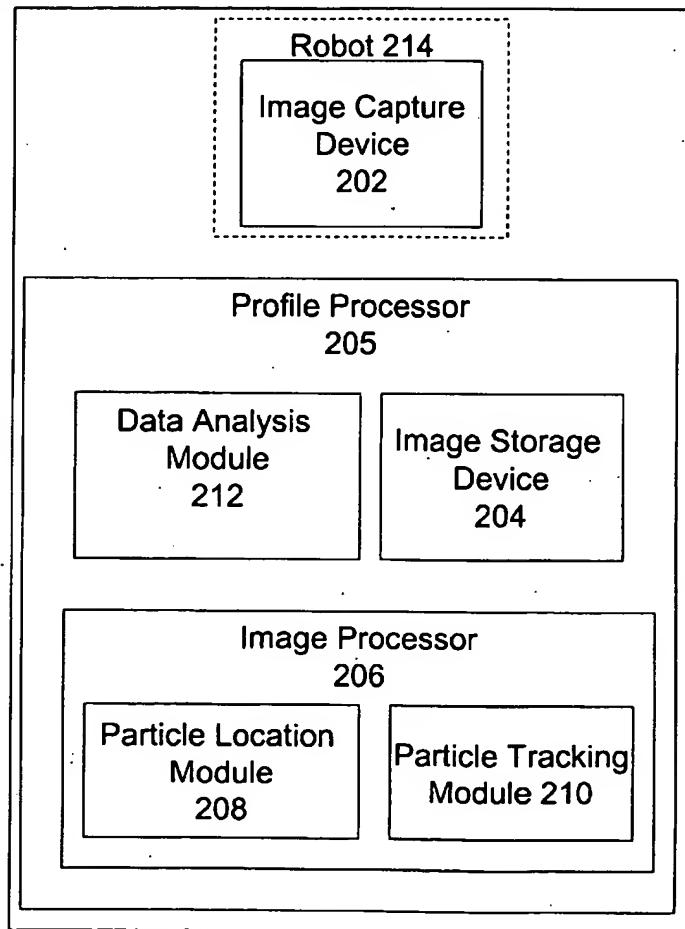
(22) **Filed: Jun. 22, 2004**

**Publication Classification**

(51) **Int. Cl.<sup>7</sup> G01F 17/00; G01F 23/00; G01L 7/00; G01N 11/00; G06F 19/00**

The invention relates to a computerized method of profiling a shear flow, such as a boundary layer. The method includes receiving two successive images of a plurality of particles in the shear flow near the interface being analyzed. The method also includes determining a set of potential particle motion vectors based on the received images and dynamically ranks the likelihood that the potential tracks are correct based on track density. Track density is calculated using a plot matrix and kernel technique. The ranking is used to match particles from the successive images. The method also includes generating a velocity profile of the flow about the interface based on the particles matches and the determined location of the interface. The method is also applicable to moving and deforming interfaces.

200



Summary of Invention Paragraph:

[0020] Brooks, D. E. and Trust, T. J. (1983) "Enhancement of bacterial adhesion by shear forces: characterization of the haemagglutination induced by *Aeromonas salmonicida* strain 438," *J. Gen. Microbiol.* 129:3661-3669.

Summary of Invention Paragraph:

[0027] Christersson, C. E. et al. (1988) "Role of temperature and shear forces on microbial detachment," *Scand. J. Dent. Res.* 96:91-98.

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L9: Entry 1 of 16

File: PGPB

May 18, 2006

DOCUMENT-IDENTIFIER: US 20060106198 A1

TITLE: Antimicrobials against pathogenic bacteria and method for screening them

Description of Disclosure:

[0037] To further analyze the different Caf1M-(Caf1).sub.n complexes they were subjected to analytical gel chromatography (FIG. 3B). The K.sub.av values for the complexes were plotted against the log of the assumed MW (FIG. 3B, circles). Starting from the second complex, the dependence was linear suggesting that the MWs had been correctly estimated. However, the line obtained from the complexes, and the linear calibration obtained from standard globular proteins (FIG. 3B, squares) had different slopes. The ratio of the slopes for complexes ( $K=0.411\pm0.009$ ) and globular proteins ( $K=0.21\pm0.035$ ) was about 2. This shows that the complexes have a larger hydrodynamic radius of gyration than expected for globular proteins of similar size, indicating that Caf1M-Caf1.sub.n complexes with two or more Caf1 subunits have coil-like or flexible rod-like shapes (Yau, W. W. and Bly, D. D., 1980, in: *Size Exclusion Chromatography*, Provder, T., ed., ACS Symposium Series, American Chemical Society, Washington, D.C., pp. 197-204). The K.sub.av of the smallest complex (Caf1M-Caf1; estimated MW 44.3 kDa) did not fit well to the line obtained for higher-order complexes, but did fit to the linear calibration for globular proteins, where its MW is determined as 40-60 kDa and its K.sub.av was almost the same as that of ovalbumin (43 kDa). Assuming a similar mode of binding as observed for the PapD-PapK and FimC-FimH chaperone-subunit complexes (Sauer, F. G. et al., 1999, *Science* 285, pp. 1058-1061; Choudhury, D. et al., 1999, *Science* 285, pp. 1061-1066), the shape of the Caf1M-Caf1 complex is expected to be roughly spherical.

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1/6,KWIC/1 (Item 1 from file: 35)
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A STUDY OF THE INSECTICIDAL TOXIN GENES OF BACILLUS SPHAERICUS, STRAINS
1593, 2362 AND 2297
Year: 1988
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...this strain. In subsequent experiments, the entire coding regions for the toxins of *Bacillus sphaericus* strains 1593, 2362 and 2297 were cloned into the *Escherichia \*\*\*coli\*\*\** plasmids pUC12 and pUC13. The cloned DNA was sequenced either directly in these pUC based...

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